



1600

RAW SEQUENCE LISTING

DATE: 07/30/2002

PATENT APPLICATION: US/09/044,696B

TIME: 15:11:26

Input Set : A:\seqlist.txt

Output Set: N:\CRF3\07302002\I044696B.raw

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AUG 06 2002

TECH CENTER 1600/2900

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3 <110> APPLICANT: BARCHFELD, Gail
4     DEL GIUDICE, Giuseppe
5     RAPPUOLI, Rino
7 <120> TITLE OF INVENTION: DETOXIFIED MUTANTS OF BACTERIAL ADP-RIBOSYLATING TOXINS
8     AS PARENTERAL ADJUVANTS
10 <130> FILE REFERENCE: 2302-1393 / PP01393.002
12 <140> CURRENT APPLICATION NUMBER: 09/044,696B
13 <141> CURRENT FILING DATE: 1998-03-18
15 <160> NUMBER OF SEQ ID NOS: 5
17 <170> SOFTWARE: PatentIn Ver. 2.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 711
21 <212> TYPE: DNA
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (1)..(708)
28 <220> FEATURE:
29 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type Subunit
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32 <400> SEQUENCE: 1
33 aat ggc gac aga tta tac cgt gct gac tct aga ccc cca gat gaa ata      48
34 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
35   1             5             10             15
37 aaa cgt ttc cgg agt ctt atg ccc aga ggt aat gag tac ttc gat aga      96
38 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
39             20             25             30
41 gga act caa atg aat att aat ctt tat gat cac gcg aga gga aca caa     144
42 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
43             35             40             45
45 acc ggc ttt gtc aga tat gat gac gga tat gtt tcc act tct ctt agt     192
46 Thr Gly Phe Val Arg Tyr Asp Gly Tyr Val Ser Thr Ser Leu Ser
47             50             55             60
49 ttg aga agt gct cac tta gca gga cag tat ata tta tca gga tat tca     240
50 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
51 65             70             75             80
53 ctt act ata tat atc gtt ata gca aat atg ttt aat gtt aat gat gta     288
54 Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
55             85             90             95
57 att agc gta tac agc cct cac cca tat gaa cag gag gtt tct gcg tta     336
58 Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
59             100            105            110
61 ggt gga ata cca tat tct cag ata tat gga tgg tat cgt gtt aat ttt     384

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62 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
63      115      120      125
65 ggt gtg att gat gaa cga tta cat cgt aac agg gaa tat aga gac cgg 432
66 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
67      130      135      140
69 tat tac aga aat ctg aat ata gct ccg gca gag gat ggt tac aga tta 480
70 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
71 145      150      155      160
73 gca ggt ttc cca ccg gat cac caa gct tgg aga gaa gaa ccc tgg att 528
74 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
75      165      170      175
77 cat cat gca cca caa ggt tgt gga gat tca tca aga aca atc aca ggt 576
78 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
79      180      185      190
81 gat act tgt aat gag gag acc cag aat ctg agc aca ata tat ctc agg 624
82 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
83      195      200      205
85 gaa tat caa tca aaa gtt aag agg cag ata ttt tca gac tat cag tca 672
86 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
87      210      215      220
89 gag gtt gac ata tat aac aga att cgg gat gaa tta tga 711
90 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
91 225      230      235
94 <210> SEQ ID NO: 2
95 <211> LENGTH: 236
96 <212> TYPE: PRT
97 <213> ORGANISM: Artificial Sequence
99 <220> FEATURE:
100 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type Subunit
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103 <400> SEQUENCE: 2
104 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
105 1      5      10      15
107 Lys Arg Phe Arg Ser Leu Met Pro Arg Gly Asn Glu Tyr Phe Asp Arg
108      20      25      30
110 Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr Gln
111      35      40      45
113 Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu Ser
114      50      55      60
116 Leu Arg Ser Ala His Leu Ala Gly Gln Tyr Ile Leu Ser Gly Tyr Ser
117 65      70      75      80
119 Leu Thr Ile Tyr Ile Val Ile Ala Asn Met Phe Asn Val Asn Asp Val
120      85      90      95
122 Ile Ser Val Tyr Ser Pro His Pro Tyr Glu Gln Glu Val Ser Ala Leu
123      100      105      110
125 Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr Arg Val Asn Phe
126      115      120      125
128 Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu Tyr Arg Asp Arg
129      130      135      140

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131 Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp Gly Tyr Arg Leu
132 145 150 155 160
134 Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu Glu Pro Trp Ile
135 165 170 175
137 His His Ala Pro Gln Gly Cys Gly Asp Ser Ser Arg Thr Ile Thr Gly
138 180 185 190
140 Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr Ile Tyr Leu Arg
141 195 200 205
143 Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser Asp Tyr Gln Ser
144 210 215 220
146 Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
147 225 230 235
150 <210> SEQ ID NO: 3
151 <211> LENGTH: 723
152 <212> TYPE: DNA
153 <213> ORGANISM: Artificial Sequence
155 <220> FEATURE:
156 <221> NAME/KEY: CDS
157 <222> LOCATION: (1)..(720)
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type CT
161 subunit A
163 <400> SEQUENCE: 3
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165 Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
166 1 5 10 15
168 aag cag tca ggt ggt ctt atg cca aga gga cag agt gag tac ttt gac 96
169 Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
170 20 25 30
172 cga ggt act caa atg aat atc aac ctt tat gat cat gca aga gga act 144
173 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
174 35 40 45
176 cag acg gga ttt gtt agg cac gat gat gga tat gtt tcc acc tca att 192
177 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
178 50 55 60
180 agt ttg aga agt gcc cac tta gtg ggt caa act ata ttg tct ggt cat 240
181 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
182 65 70 75 80
184 tct act tat tat ata tat gtt ata gcc act gca ccc aac atg ttt aac 288
185 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
186 85 90 95
188 gtt aat gat gta tta ggg gca tac agt cct cat cca gat gaa caa gaa 336
189 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
190 100 105 110
192 gtt tct gct tta ggt ggg att cca tac tcc caa ata tat gga tgg tat 384
193 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
194 115 120 125
196 cga gtt cat ttt ggg gtg ctt gat gaa caa tta cat cgt aat agg ggc 432
197 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly

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198      130      135      140
200 tac aga gat aga tat tac agt aac tta gat att gct cca gca gca gat 480
201 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
202 145      150      155      160
204 ggt tat gga ttg gca ggt ttc cct ccg gag cat aga gct tgg agg gaa 528
205 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu
206      165      170      175
208 gag ccg tgg att cat cat gca ccg ccg ggt tgt ggg aat gct cca aga 576
209 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
210      180      185      190
212 tca tcg atc agt aat act tgc gat gaa aaa acc caa agt cta ggt gta 624
213 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
214      195      200      205
216 aaa ttc ctt gac gaa tac caa tct aaa gtt aaa aga caa ata ttt tca 672
217 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
218      210      215      220
220 ggc tat caa tct gat att gat aca cat aat aga att aag gat gaa tta 720
221 Gly Tyr Gln Ser Asp Ile Asp Thr His Asn Arg Ile Lys Asp Glu Leu
222 225      230      235      240
224 tga 723
227 <210> SEQ ID NO: 4
228 <211> LENGTH: 240
229 <212> TYPE: PRT
230 <213> ORGANISM: Artificial Sequence
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Description of Artificial Sequence: wild-type CT
234 subunit A
236 <400> SEQUENCE: 4
237 Asn Asp Asp Lys Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
238 1 5 10 15
240 Lys Gln Ser Gly Gly Leu Met Pro Arg Gly Gln Ser Glu Tyr Phe Asp
241 20 25 30
243 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
244 35 40 45
246 Gln Thr Gly Phe Val Arg His Asp Asp Gly Tyr Val Ser Thr Ser Ile
247 50 55 60
249 Ser Leu Arg Ser Ala His Leu Val Gly Gln Thr Ile Leu Ser Gly His
250 65 70 75 80
252 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
253 85 90 95
255 Val Asn Asp Val Leu Gly Ala Tyr Ser Pro His Pro Asp Glu Gln Glu
256 100 105 110
258 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
259 115 120 125
261 Arg Val His Phe Gly Val Leu Asp Glu Gln Leu His Arg Asn Arg Gly
262 130 135 140
264 Tyr Arg Asp Arg Tyr Tyr Ser Asn Leu Asp Ile Ala Pro Ala Ala Asp
265 145 150 155 160
267 Gly Tyr Gly Leu Ala Gly Phe Pro Pro Glu His Arg Ala Trp Arg Glu

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268          165          170          175
270 Glu Pro Trp Ile His His Ala Pro Pro Gly Cys Gly Asn Ala Pro Arg
271          180          185          190
273 Ser Ser Ile Ser Asn Thr Cys Asp Glu Lys Thr Gln Ser Leu Gly Val
274          195          200          205
276 Lys Phe Leu Asp Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
277          210          215          220
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288 <220> FEATURE:
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290      A from E. coli heat labile toxin
292 <400> SEQUENCE: 5
293 Asn Gly Asp Arg Leu Tyr Arg Ala Asp Ser Arg Pro Pro Asp Glu Ile
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296 Lys Arg Ser Gly Gly Leu Met Pro Arg Gly His Asn Glu Tyr Phe Asp
297          20          25          30
299 Arg Gly Thr Gln Met Asn Ile Asn Leu Tyr Asp His Ala Arg Gly Thr
300          35          40          45
302 Gln Thr Gly Phe Val Arg Tyr Asp Asp Gly Tyr Val Ser Thr Ser Leu
303          50          55          60
305 Ser Leu Arg Ser Ala His Leu Ala Gly Gln Ser Ile Leu Ser Gly Tyr
306 65          70          75          80
308 Ser Thr Tyr Tyr Ile Tyr Val Ile Ala Thr Ala Pro Asn Met Phe Asn
309          85          90          95
311 Val Asn Asp Val Leu Gly Val Tyr Ser Pro His Pro Tyr Glu Gln Glu
312          100          105          110
314 Val Ser Ala Leu Gly Gly Ile Pro Tyr Ser Gln Ile Tyr Gly Trp Tyr
315          115          120          125
317 Arg Val Asn Phe Gly Val Ile Asp Glu Arg Leu His Arg Asn Arg Glu
318          130          135          140
320 Tyr Arg Asp Arg Tyr Tyr Arg Asn Leu Asn Ile Ala Pro Ala Glu Asp
321 145          150          155          160
323 Gly Tyr Arg Leu Ala Gly Phe Pro Pro Asp His Gln Ala Trp Arg Glu
324          165          170          175
326 Glu Pro Trp Ile His His Ala Pro Gln Gly Cys Gly Asn Ser Ser Arg
327          180          185          190
329 Thr Ile Thr Gly Asp Thr Cys Asn Glu Glu Thr Gln Asn Leu Ser Thr
330          195          200          205
332 Ile Tyr Leu Arg Glu Tyr Gln Ser Lys Val Lys Arg Gln Ile Phe Ser
333          210          215          220
335 Asp Tyr Gln Ser Glu Val Asp Ile Tyr Asn Arg Ile Arg Asp Glu Leu
336 225          230          235          240

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